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SIGNATURES OF SELECTION IN THE GRAPEVINE FLOWERING GENE NETWORK

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Flowering time is a complex trait important for crop improvement. Recently, by using progenies derived from different crosses of grapevine varieties, a new QTL for this trait was mapped in the grape genome. Here, we resequenced six candidate flowering genes located in this QTL from a subset of grapevine accessions representative of the FEM germplasm collection. These genes cooperate to regulate meristem formation and flowering transition. The population structure analysis based on reference SNP markers spread across the genome detected three subpopulations in this sample, and it is consistent with the eco-geographical origin of the cultivars. The level of genetic diversity within the QTL region suggests that these flowering genes are targets of selection. In this work, we will discuss possible genotype-phenotype relationships for these candidate genes, investigated by applying field observations of flowering time in the core collection, recorded during several years. This might allow us to facilitate choice of grapevine varieties adapted to atmospheric conditions of a specific geographic location.